~~Fig. 2b is the nucleotide sequence of GFP (SEQ ID NO:21);~~

Fig. 3 is the DNA (SEQ ID NO:15) and predicted amino acid sequence (SEQ ID NO:16) of F64L-Y66H-GFP;

Fig. 4 is the DNA (SEQ ID NO:17) and predicted amino acid sequence (SEQ ID NO:18) of F64L-GFP;

Fig. 5 is the DNA (SEQ ID NO:19) and predicted amino acid sequence (SEQ ID ~~NO:20) of F64L-S65T-GFP;~~

Please replace the paragraph beginning on page 12, line 25, with the following rewritten paragraph:

--Briefly, total RNA, isolated from A. victoria by a standard procedure (Sambrook et al., Molecular Cloning. 2., eds. (1989) (Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York), 7.19-7.22) was converted into cDNA by using the AMV reverse transcriptase (Promega, Madison, WI, USA) as recommended by the manufacturer. The cDNA was then PCR amplified, using PCR primers designed on the basis of a previously published GFP sequence (Prasher et al., Gene 111 (1992), 229-223; GenBank accession No. M62653) together with the UlTmaTM polymerase (Perkin Elmer, Foster City, CA, USA). The sequences of the primers were: GFP2: TGGAATAAGCTTTATGAGTAAAGGAGAAGAACTTTT (SEQ ID NO:1) and GFP-1:AAGAATTCGGATCCCTTTAGTGTCAATTGGAAGTCT (SEQ ID NO:2) Restriction endonuclease sites inserted in the 5' (a HindIII site) and 3' (EcoRI and BamHI sites) primers facilitated the cloning of the PCR amplified GFP cDNA into a slightly modified pUC19 vector. The details of the construction are as follows: LacZ

Shine-Dalgarno AGGA, immediately followed by the 5' HindIII site plus an extra T and the GFP ATG codon, giving the following DNA sequence at the lacZ-promoter GFP fusion point:~P_{Lacz}-AGGAAAGCTTTATG-GFP (SEQ ID NO:23). At the 3' end of the GFP cDNA, the base pair corresponding to nucleotide 770 in the published GFP sequence (GenBank accession No. M62653) was fused to the EcoRI site of the pUC19 multiple cloning site (MCS) through a PCR generated BamHI, EcoRI linker region).

Please delete the Substitute Sequence Listing filed August 12, 2002, pages numbered 1-3. Please insert the attached Second Substitute Sequence Listing, independently numbered pages 1-14 directly after the abstract.